



SEQUENCE LISTING

<110> ASAKO, HIROYUKI
MATSUMURA, KENJI
SHIMIZU, MASATOSHI
ITO, NOBUYA
WAKITA, RYUHEI

<120> PROCESS FOR PRODUCING OPTICALLY ACTIVE
4-HALO-3-HYDROXYBUTANOATE

<130> 7372-72249

<140> 10/004,115

<141> 2001-12-06

<150> JP 2000-372704

<151> 2000-12-07

<150> JP 2001-006144

<151> 2001-01-15

<150> JP 2001-026594

<151> 2001-02-02

<150> JP 2001-175175

<151> 2001-06-11

<160> 37

<170> PatentIn Ver. 2.1

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<212> PRT

<213> Penicillium citrinum

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35 40 45

Cys Ala Trp Tyr Tyr Leu Asn Glu Gly Glu Val Gly Glu Gly Ile Arg
50 55 60

Asp Phe Leu Lys Glu Asn Pro Ser Val Lys Arg Glu Asp Ile Phe Val
65 70 75 80

Cys Thr Lys Val Trp Asn His Leu His Arg Tyr Glu Asp Val Leu Trp
85 90 95

Ser Ile Asp Asp Ser Leu Lys Arg Leu Gly Leu Asp Tyr Val Asp Met
100 105 110

Phe Leu Val His Trp Pro Ile Ala Ala Glu Lys Asn Gly Gln Gly Glu
 115 120 125
 Pro Lys Ile Gly Pro Asp Gly Lys Tyr Val Ile Leu Lys Asp Leu Thr
 130 135 140
 Glu Asn Pro Glu Pro Thr Trp Arg Ala Met Glu Lys Ile Tyr Glu Asp
 145 150 155 160
 Arg Lys Ala Arg Ser Ile Gly Val Ser Asn Trp Thr Ile Ala Asp Leu
 165 170 175
 Glu Lys Met Ser Lys Phe Ala Lys Val Met Pro His Ala Asn Gln Ile
 180 185 190
 Glu Ile His Pro Phe Leu Pro Asn Glu Glu Leu Val Gln Tyr Cys Phe
 195 200 205
 Ser Lys Asn Ile Met Pro Val Ala Tyr Ser Pro Leu Gly Ser Gln Asn
 210 215 220
 Gln Val Pro Thr Thr Gly Glu Arg Val Ser Glu Asn Lys Thr Leu Asn
 225 230 235 240
 Glu Ile Ala Glu Lys Gly Gly Asn Thr Leu Ala Gln Val Leu Ile Ala
 245 250 255
 Trp Gly Leu Arg Arg Gly Tyr Val Val Leu Pro Lys Ser Ser Asn Pro
 260 265 270
 Lys Arg Ile Glu Ser Asn Phe Lys Ser Ile Glu Leu Ser Asp Ala Asp
 275 280 285
 Phe Glu Ala Ile Asn Ala Val Ala Lys Gly Arg His Phe Arg Phe Val
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ggc gtc ggc ttt ggt acc ttc gct agt gaa ggt tcc aag ggc gag acc	96
Gly Val Gly Phe Gly Thr Phe Ala Ser Glu Gly Ser Lys Gly Glu Thr	
20 25 30	
tat act gct gtc acc act gcc ctg aag acc ggt tac cgt cac ttg gac	144
Tyr Thr Ala Val Thr Thr Ala Leu Lys Thr Gly Tyr Arg His Leu Asp	
35 40 45	
tgt gcc tgg tac tac ctg aac gag ggt gag gtt ggt gag ggt atc cgt	192
Cys Ala Trp Tyr Tyr Leu Asn Glu Gly Glu Val Gly Glu Gly Ile Arg	
50 55 60	
gac ttc ctg aag gag aac ccc tcg gtg aag cgt gag gac atc ttc gtc	240
Asp Phe Leu Lys Glu Asn Pro Ser Val Lys Arg Glu Asp Ile Phe Val	
65 70 75 80	
tgc acc aag gtg tgg aac cac ctc cac cgt tat gag gac gtc ctc tgg	288
Cys Thr Lys Val Trp Asn His Leu His Arg Tyr Glu Asp Val Leu Trp	
85 90 95	
tcc att gac gac tcc ctg aag cgt ctt gga ctt gac tac gtt gat atg	336
Ser Ile Asp Asp Ser Leu Lys Arg Leu Gly Leu Asp Tyr Val Asp Met	
100 105 110	
ttc ctc gtt cac tgg ccc att gct gcc gag aag aat ggc cag ggt gag	384
Phe Leu Val His Trp Pro Ile Ala Ala Glu Lys Asn Gly Gln Gly Glu	
115 120 125	
ccc aag att ggc cct gac ggc aaa tac gtc att ctc aag gac ctg acc	432
Pro Lys Ile Gly Pro Asp Gly Lys Tyr Val Ile Leu Lys Asp Leu Thr	
130 135 140	
gag aac ccc gag ccc aca tgg cgc gct atg gag aag att tat gag gat	480
Glu Asn Pro Glu Pro Thr Trp Arg Ala Met Glu Lys Ile Tyr Glu Asp	
145 150 155 160	
cgc aag gcc agg tcc att ggt gtc tcc aac tgg acc att gcc gac ctt	528
Arg Lys Ala Arg Ser Ile Gly Val Ser Asn Trp Thr Ile Ala Asp Leu	
165 170 175	
gag aag atg tcc aag ttc gcc aag gtc atg cct cac gcc aac cag atc	576
Glu Lys Met Ser Lys Phe Ala Lys Val Met Pro His Ala Asn Gln Ile	
180 185 190	
gag att cac ccc ttc ctg ccc aac gag gag ctg gtg cag tac tgc ttc	624
Glu Ile His Pro Phe Leu Pro Asn Glu Glu Leu Val Gln Tyr Cys Phe	
195 200 205	
tcc aag aac att atg ccc gtg gcc tac tct cct ctg ggc tcg cag aac	672
Ser Lys Asn Ile Met Pro Val Ala Tyr Ser Pro Leu Gly Ser Gln Asn	
210 215 220	
cag gtt ccc acc acc ggt gag cgg gtc agc gag aac aag act ctg aac	720
Gln Val Pro Thr Thr Gly Glu Arg Val Ser Glu Asn Lys Thr Leu Asn	
225 230 235 240	

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 Glu Ile Ala Glu Lys Gly Gly Asn Thr Leu Ala Gln Val Leu Ile Ala
 245 250 255

tgg ggt ctg cgc cgt ggc tac gtc gtt ctc ccc aag agc tcc aac ccc 816
 Trp Gly Leu Arg Arg Gly Tyr Val Val Leu Pro Lys Ser Ser Asn Pro
 260 265 270

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 Lys Arg Ile Glu Ser Asn Phe Lys Ser Ile Glu Leu Ser Asp Ala Asp
 275 280 285

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 Phe Glu Ala Ile Asn Ala Val Ala Lys Gly Arg His Phe Arg Phe Val
 290 295 300

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 <212> PRT
 <213> Penicillium citrinum

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<210> 4
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 <213> Artificial Sequence

<220>
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<220>
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<212> DNA
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<220>
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 agtgaagggt ccaagggcga aacctatnct gctgtcacca ctgccctgaa aaccgggttac 180
 cgtcncttgg actgtgcctg gtactacctg aacaagggtg aggttggtga gggtnccgt 240
 gacttctga aggaaaaccc ctcggtgaag cgtgaggaca tcttcgtctg caccaagggtg 300
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gaaancccnna ncccacctgg cgcgctatgg aaaaaatttn tgangatccc aaggccaggt 540
ccattgggtgt ttccaattgg accattgccg accttgagaa gatgtccaag ttngccaagg 600
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<210> 16

<211> 21

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Primer

<400> 16

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<210> 17

<211> 20

<212> DNA

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<223> Description of Artificial Sequence: Primer

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<210> 18

<211> 331

<212> DNA

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ggctttggta cttcgctag tgaagggtcc aagggcgaga cctatactgc tgtcaccact 180
gccctgaaga cgggttaccg tcaactggac tgtgcctggg actacctgaa cgaggggtgag 240
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<212> DNA

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 cggtgagcgg gtcagcgaga acaagactct gaacgagatc gccgagaagg gcggcaacac 180
 ccttgctcag gttcttattg cctgggggtct gcgccgtggc tacgtcgttc tccccaagag 240
 ctccaacccc aagcgcattg agtccaactt caagagcatt gagctctccg atgccgactt 300
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 ttctcgatat gatgtctggc ccgaggagac cgccaagaac ctgtctgcgt gaatctctac 420
 gaaattataa aatnacaccn acnaaaancc aaagcganag gatgatnccc aaaanttttg 480
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 caattcnccc cttatnattg aattcttttt taanggggnc aaattccncc nnatttcnt 660
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 aantggantt cctntttacc ttt 743

<210> 20
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 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Primer

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<210> 21
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Primer

<400> 21
 ccagaggaga gtaggccacg g 21

<210> 22
 <211> 417
 <212> DNA
 <213> Escherichia coli

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 tcgccaaggt catgcctcac gccaaaccaga tcgagattca ccccttcctg cccaacgagg 360
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 <213> Artificial Sequence

<220>
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<210> 24
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<223> Description of Artificial Sequence: Primer

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29

<210> 25

<211> 21

<212> DNA

<213> Artificial Sequence

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<210> 26

<211> 21

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Primer

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<210> 27

<211> 786

<212> DNA

<213> Escherichia coli

<220>

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<222> (1)..(783)

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acc	ggt	tta	gga	aaa	gca	atg	gcg	att	cgt	ttt	gcg	aca	gaa	aaa	gct	96
Thr	Gly	Leu	Gly	Lys	Ala	Met	Ala	Ile	Arg	Phe	Ala	Thr	Glu	Lys	Ala	
		20					25					30				

aaa	gta	gtt	gtg	aac	tat	cgt	tcg	aaa	gaa	gaa	gaa	gct	aac	agc	gtt	144
Lys	Val	Val	Val	Asn	Tyr	Arg	Ser	Lys	Glu	Glu	Glu	Ala	Asn	Ser	Val	
		35					40					45				

tta	gaa	gaa	att	aaa	aaa	gtg	ggc	gga	gag	gct	att	gcc	gtc	aaa	ggt	192
Leu	Glu	Glu	Ile	Lys	Lys	Val	Gly	Gly	Glu	Ala	Ile	Ala	Val	Lys	Gly	
		50				55					60					

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65 70 75 80	
aaa gaa ttt gga aag cta gac gtt atg att aat aac gca gga atg gaa	288
Lys Glu Phe Gly Lys Leu Asp Val Met Ile Asn Asn Ala Gly Met Glu	
85 90 95	
aat ccg gtt tcg tct cat gaa atg tct tta agt gat tgg aat aaa gtc	336
Asn Pro Val Ser Ser His Glu Met Ser Leu Ser Asp Trp Asn Lys Val	
100 105 110	
att gat acg aac tta acg gga gca ttt tta ggc agc cgt gaa gcg att	384
Ile Asp Thr Asn Leu Thr Gly Ala Phe Leu Gly Ser Arg Glu Ala Ile	
115 120 125	
aaa tat ttt gtg gaa aat gat att aag gga aca gtt att aac atg tcg	432
Lys Tyr Phe Val Glu Asn Asp Ile Lys Gly Thr Val Ile Asn Met Ser	
130 135 140	
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Ser Val His Glu Lys Ile Pro Trp Pro Leu Phe Val His Tyr Ala Ala	
145 150 155 160	
agt aaa ggc gga atg aag ctc atg acc gaa aca ctt gca tta gaa tac	528
Ser Lys Gly Gly Met Lys Leu Met Thr Glu Thr Leu Ala Leu Glu Tyr	
165 170 175	
gct cca aaa ggt att cgt gta aat aac att gga ccg gga gcg att aat	576
Ala Pro Lys Gly Ile Arg Val Asn Asn Ile Gly Pro Gly Ala Ile Asn	
180 185 190	
aca ccg att aac gct gag aaa ttt gct gat cct gag cag cgt gca gat	624
Thr Pro Ile Asn Ala Glu Lys Phe Ala Asp Pro Glu Gln Arg Ala Asp	
195 200 205	
gta gaa agc atg att cca atg gga tac att gga gag ccg gaa gaa att	672
Val Glu Ser Met Ile Pro Met Gly Tyr Ile Gly Glu Pro Glu Glu Ile	
210 215 220	
gca gcg gtt gct gca tgg cta gct tct tca gag gca agt tat gta aca	720
Ala Ala Val Ala Ala Trp Leu Ala Ser Ser Glu Ala Ser Tyr Val Thr	
225 230 235 240	
ggg att aca ctc ttt gct gac ggc ggt atg aca cag tac cca tca ttc	768
Gly Ile Thr Leu Phe Ala Asp Gly Gly Met Thr Gln Tyr Pro Ser Phe	
245 250 255	
caa gca gga cgc gga taa	786
Gln Ala Gly Arg Gly	
260	

<210> 28

<211> 996

<212> DNA

<213> Penicillium citrinum

<220>

<221> CDS

<222> (1)..(975)

<400> 28

atg tct aac gga aag act ttc aca ttg agc aac ggc gtc aag att cct	48
Met Ser Asn Gly Lys Thr Phe Thr Leu Ser Asn Gly Val Lys Ile Pro	
1 5 10 15	
ggc gtc ggc ttt ggt acc ttc gct agt gaa ggt tcc aag ggc gag acc	96
Gly Val Gly Phe Gly Thr Phe Ala Ser Glu Gly Ser Lys Gly Glu Thr	
20 25 30	
tat act gct gtc acc act gcc ctg aag acc ggt tac cgt cac ttg gac	144
Tyr Thr Ala Val Thr Thr Ala Leu Lys Thr Gly Tyr Arg His Leu Asp	
35 40 45	
tgt gcc tgg tac tac ctg aac gag ggt gag gtt ggt gag ggt atc cgt	192
Cys Ala Trp Tyr Tyr Leu Asn Glu Gly Glu Val Gly Glu Gly Ile Arg	
50 55 60	
gac ttc ctg aag gag aac ccc tcg gtg aag cgt gag gac atc ttc gtc	240
Asp Phe Leu Lys Glu Asn Pro Ser Val Lys Arg Glu Asp Ile Phe Val	
65 70 75 80	
tgc acc aag gtg tgg aac cac ctc cac cgt tat gag gac gtc ctc tgg	288
Cys Thr Lys Val Trp Asn His Leu His Arg Tyr Glu Asp Val Leu Trp	
85 90 95	
tcc att gac gac tcc ctg aag cgt ctt gga ctt gac tac gtt gat atg	336
Ser Ile Asp Asp Ser Leu Lys Arg Leu Gly Leu Asp Tyr Val Asp Met	
100 105 110	
ttc ctc gtt cac tgg ccc att gct gcc gag aag aat ggc cag ggt gag	384
Phe Leu Val His Trp Pro Ile Ala Ala Glu Lys Asn Gly Gln Gly Glu	
115 120 125	
ccc aag att ggc cct gac ggc aaa tac gtc att ctc aag gac ctg acc	432
Pro Lys Ile Gly Pro Asp Gly Lys Tyr Val Ile Leu Lys Asp Leu Thr	
130 135 140	
gag aac ccc gag ccc aca tgg cgc gct atg gag aag att tat gag gat	480
Glu Asn Pro Glu Pro Thr Trp Arg Ala Met Glu Lys Ile Tyr Glu Asp	
145 150 155 160	
cgc aag gcc agg tcc att ggt gtc tcc aac tgg acc att gcc gac ctt	528
Arg Lys Ala Arg Ser Ile Gly Val Ser Asn Trp Thr Ile Ala Asp Leu	
165 170 175	
gag aag atg tcc aag ttc gcc aag gtc atg cct cac gcc aac cag atc	576
Glu Lys Met Ser Lys Phe Ala Lys Val Met Pro His Ala Asn Gln Ile	
180 185 190	
gag att cac ccc ttc ctg ccc aac gag gag ctg gtg cag tac tgc ttc	624
Glu Ile His Pro Phe Leu Pro Asn Glu Glu Leu Val Gln Tyr Cys Phe	
195 200 205	

tcc aag aac att atg ccc gtg gcc tac tct cct ctg ggc tcg cag aac	672
Ser Lys Asn Ile Met Pro Val Ala Tyr Ser Pro Leu Gly Ser Gln Asn	
210 215 220	
cag gtt ccc acc acc ggt gag cgg gtc agc gag aac aag act ctg aac	720
Gln Val Pro Thr Thr Gly Glu Arg Val Ser Glu Asn Lys Thr Leu Asn	
225 230 235 240	
gag atc gcc gag aag ggc ggc aac acc ctt gct cag gtt ctt att gcc	768
Glu Ile Ala Glu Lys Gly Gly Asn Thr Leu Ala Gln Val Leu Ile Ala	
245 250 255	
tgg ggt ctg cgc cgt ggc tac gtc gtt ctc ccc aag agc tcc aac ccc	816
Trp Gly Leu Arg Arg Gly Tyr Val Val Leu Pro Lys Ser Ser Asn Pro	
260 265 270	
aag cgc att gag tcc aac ttc aag agc att gag ctc tcc gat gcc gac	864
Lys Arg Ile Glu Ser Asn Phe Lys Ser Ile Glu Leu Ser Asp Ala Asp	
275 280 285	
ttt gaa gcc atc aat gcc gtt gcc aag ggt cgt cac ttc cgt ttc gtc	912
Phe Glu Ala Ile Asn Ala Val Ala Lys Gly Arg His Phe Arg Phe Val	
290 295 300	
aac atg aag gat act ttc gga tat gat gtc tgg ccc gag gag acc gcc	960
Asn Met Lys Asp Thr Phe Gly Tyr Asp Val Trp Pro Glu Glu Thr Ala	
305 310 315 320	
aag aac ctg tct gcg tgaatctcta cgaaattata a	996
Lys Asn Leu Ser Ala	
325	

<210> 29

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 29

cggatccggtt cacgcagaca gggtcttgg

29

<210> 30

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 30

gccatggcta tgtataaaga tttagaa

27

<210> 31

<400> 31
000

<210> 32

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 32

cggatccggtt atccgcgtcc tgc

23

<210> 33

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 33

cggatccgag cgccaatac gcaaaccg

28

<210> 34

<211> 385

<212> PRT

<213> Corynebacterium sp.

<400> 34

Met Lys Ala Ile Gln Tyr Thr Arg Ile Gly Ala Glu Pro Glu Leu Thr
1 5 10 15

Glu Ile Pro Lys Pro Glu Pro Gly Pro Gly Glu Val Leu Leu Glu Val
20 25 30

Thr Ala Ala Gly Val Cys His Ser Asp Asp Phe Ile Met Ser Leu Pro
35 40 45

Glu Glu Gln Tyr Thr Tyr Gly Leu Pro Leu Thr Leu Gly His Glu Gly
50 55 60

Ala Gly Lys Val Ala Ala Val Gly Glu Gly Val Glu Gly Leu Asp Ile
65 70 75 80

Gly Thr Asn Val Val Val Tyr Gly Pro Trp Gly Cys Gly Asn Cys Trp
85 90 95

His Cys Ser Gln Gly Leu Glu Asn Tyr Cys Ser Arg Ala Gln Glu Leu
100 105 110

Gly Ile Asn Pro Pro Gly Leu Gly Ala Pro Gly Ala Leu Ala Glu Phe
 115 120 125
 Met Ile Val Asp Ser Pro Arg His Leu Val Pro Ile Gly Asp Leu Asp
 130 135 140
 Pro Val Lys Thr Val Pro Leu Thr Asp Ala Gly Leu Thr Pro Tyr His
 145 150 155 160
 Ala Ile Lys Arg Ser Leu Pro Lys Leu Arg Gly Gly Ser Tyr Ala Val
 165 170 175
 Val Ile Gly Thr Gly Gly Leu Gly His Val Ala Ile Gln Leu Leu Arg
 180 185 190
 His Leu Ser Ala Ala Thr Val Ile Ala Leu Asp Val Ser Ala Asp Lys
 195 200 205
 Leu Glu Leu Ala Thr Lys Val Gly Ala His Glu Val Val Leu Ser Asp
 210 215 220
 Lys Asp Ala Ala Glu Asn Val Arg Lys Ile Thr Gly Ser Gln Gly Ala
 225 230 235 240
 Ala Leu Val Leu Asp Phe Val Gly Tyr Gln Pro Thr Ile Asp Thr Ala
 245 250 255
 Met Ala Val Ala Gly Val Gly Ser Asp Val Thr Ile Val Gly Ile Gly
 260 265 270
 Asp Gly Gln Ala His Ala Lys Val Gly Phe Phe Gln Ser Pro Tyr Glu
 275 280 285
 Ala Ser Val Thr Val Pro Tyr Trp Gly Ala Arg Asn Glu Leu Ile Glu
 290 295 300
 Leu Ile Asp Leu Ala His Ala Gly Ile Phe Asp Ile Gly Gly Gly Asp
 305 310 315 320
 Leu Gln Ser Arg Gln Arg Cys Arg Ser Val Ser Thr Thr Gly Cys Arg
 325 330 335
 Asn Ala Gln Arg Pro Cys Gly Cys Gly Pro Trp Ser Val Val Pro Thr
 340 345 350
 Ala Val Glu Arg Gln Arg Lys Asn Thr Asp Ala Arg Pro Asn Ser Ile
 355 360 365
 Arg Pro Gly Ile Ser Val Arg Asn Ser Val Cys Ala Ser Cys Thr Pro
 370 375 380
 Arg
 385

<210> 35

<211> 1158

<212> DNA

<213> Corynebacterium sp.

<220>

<221> CDS

<222> (1)..(1155)

<400> 35

atg aag gcg atc cag tac acg cga atc ggc gcg gaa ccc gaa ctc acg	48
Met Lys Ala Ile Gln Tyr Thr Arg Ile Gly Ala Glu Pro Glu Leu Thr	
1 5 10 15	
gag att ccc aaa ccc gag ccc ggt cca ggt gaa gtg ctc ctg gaa gtc	96
Glu Ile Pro Lys Pro Glu Pro Gly Pro Gly Glu Val Leu Leu Glu Val	
20 25 30	
acc gct gct ggc gtc tgc cac tcg gac gac ttc atc atg agc ctg ccc	144
Thr Ala Ala Gly Val Cys His Ser Asp Asp Phe Ile Met Ser Leu Pro	
35 40 45	
gaa gag cag tac acc tac ggc ctt ccg ctc acg ctc ggc cac gaa ggc	192
Glu Glu Gln Tyr Thr Tyr Gly Leu Pro Leu Thr Leu Gly His Glu Gly	
50 55 60	
gca ggc aag gtc gcc gcc gtc ggc gag ggt gtc gaa ggt ctc gac atc	240
Ala Gly Lys Val Ala Ala Val Gly Glu Gly Val Glu Gly Leu Asp Ile	
65 70 75 80	
gga acc aat gtc gtc gtc tac ggg cct tgg ggt tgc ggc aac tgt tgg	288
Gly Thr Asn Val Val Val Tyr Gly Pro Trp Gly Cys Gly Asn Cys Trp	
85 90 95	
cac tgc tca caa gga ctc gag aac tat tgc tct cgc gcc caa gaa ctc	336
His Cys Ser Gln Gly Leu Glu Asn Tyr Cys Ser Arg Ala Gln Glu Leu	
100 105 110	
gga atc aat cct ccc ggt ctc ggt gca ccc ggc gcg ttg gcc gag ttc	384
Gly Ile Asn Pro Pro Gly Leu Gly Ala Pro Gly Ala Leu Ala Glu Phe	
115 120 125	
atg atc gtc gat tct cct cgc cac ctt gtc ccg atc ggt gac ctc gac	432
Met Ile Val Asp Ser Pro Arg His Leu Val Pro Ile Gly Asp Leu Asp	
130 135 140	
ccg gtc aag acg gtg ccg ctg acc gac gcc ggt ctg acg ccg tat cac	480
Pro Val Lys Thr Val Pro Leu Thr Asp Ala Gly Leu Thr Pro Tyr His	
145 150 155 160	
gcg atc aag cgt tct ctg ccg aaa ctt cgc gga ggc tcg tac gcg gtt	528
Ala Ile Lys Arg Ser Leu Pro Lys Leu Arg Gly Gly Ser Tyr Ala Val	
165 170 175	
gtc att ggt acc ggc ggt ctc ggc cac gtc gct att cag ctc ctc cgc	576
Val Ile Gly Thr Gly Gly Leu Gly His Val Ala Ile Gln Leu Leu Arg	
180 185 190	

cac ctc tcg gcg gca acg gtc atc gct ttg gac gtg agc gcg gac aag	624
His Leu Ser Ala Ala Thr Val Ile Ala Leu Asp Val Ser Ala Asp Lys	
195 200 205	
ctc gaa ctg gca acc aag gta ggc gct cac gaa gtg gtt ctg tcc gac	672
Leu Glu Leu Ala Thr Lys Val Gly Ala His Glu Val Val Leu Ser Asp	
210 215 220	
aag gac gcg gcc gag aac gtc cgc aag atc act gga agt caa ggc gcc	720
Lys Asp Ala Ala Glu Asn Val Arg Lys Ile Thr Gly Ser Gln Gly Ala	
225 230 235 240	
gca ttg gtt ctc gac ttc gtc ggc tac cag ccc acc atc gac acc gcg	768
Ala Leu Val Leu Asp Phe Val Gly Tyr Gln Pro Thr Ile Asp Thr Ala	
245 250 255	
atg gct gtc gcc ggc gtc gga tca gac gtc acg atc gtc ggg atc ggg	816
Met Ala Val Ala Gly Val Gly Ser Asp Val Thr Ile Val Gly Ile Gly	
260 265 270	
gac ggc cag gcc cac gcc aaa gtc ggg ttc ttc caa agt cct tac gag	864
Asp Gly Gln Ala His Ala Lys Val Gly Phe Phe Gln Ser Pro Tyr Glu	
275 280 285	
gct tcg gtg aca gtt ccg tat tgg ggt gcc cgc aac gag ttg atc gaa	912
Ala Ser Val Thr Val Pro Tyr Trp Gly Ala Arg Asn Glu Leu Ile Glu	
290 295 300	
ttg atc gac ctc gcc cac gcc ggc atc ttc gac atc ggc ggt gga gac	960
Leu Ile Asp Leu Ala His Ala Gly Ile Phe Asp Ile Gly Gly Gly Asp	
305 310 315 320	
ctt cag tct cga caa cgg tgc cga agc gta tcg acg act ggc tgc cgg	1008
Leu Gln Ser Arg Gln Arg Cys Arg Ser Val Ser Thr Thr Gly Cys Arg	
325 330 335	
aac gct cag cgg ccg tgc ggt tgt ggt ccc tgg tct gta gta ccg aca	1056
Asn Ala Gln Arg Pro Cys Gly Cys Gly Pro Trp Ser Val Val Pro Thr	
340 345 350	
gcg gta gaa cga cag cgg aaa aac act gat gcc cgg ccg aat tcg att	1104
Ala Val Glu Arg Gln Arg Lys Asn Thr Asp Ala Arg Pro Asn Ser Ile	
355 360 365	
cgg ccg ggc atc agt gtc aga aat tcg gtg tgc gct agc tgc acg cct	1152
Arg Pro Gly Ile Ser Val Arg Asn Ser Val Cys Ala Ser Cys Thr Pro	
370 375 380	
cga tga	1158
Arg	
385	

<210> 36

<211> 261

<212> PRT

<213> Escherichia coli

<400> 36

Met Tyr Lys Asp Leu Glu Gly Lys Val Val Val Ile Thr Gly Ser Ser
 1 5 10 15
 Thr Gly Leu Gly Lys Ala Met Ala Ile Arg Phe Ala Thr Glu Lys Ala
 20 25 30
 Lys Val Val Val Asn Tyr Arg Ser Lys Glu Glu Glu Ala Asn Ser Val
 35 40 45
 Leu Glu Glu Ile Lys Lys Val Gly Gly Glu Ala Ile Ala Val Lys Gly
 50 55 60
 Asp Val Thr Val Glu Ser Asp Val Ile Asn Leu Val Gln Ser Ala Ile
 65 70 75 80
 Lys Glu Phe Gly Lys Leu Asp Val Met Ile Asn Asn Ala Gly Met Glu
 85 90 95
 Asn Pro Val Ser Ser His Glu Met Ser Leu Ser Asp Trp Asn Lys Val
 100 105 110
 Ile Asp Thr Asn Leu Thr Gly Ala Phe Leu Gly Ser Arg Glu Ala Ile
 115 120 125
 Lys Tyr Phe Val Glu Asn Asp Ile Lys Gly Thr Val Ile Asn Met Ser
 130 135 140
 Ser Val His Glu Lys Ile Pro Trp Pro Leu Phe Val His Tyr Ala Ala
 145 150 155 160
 Ser Lys Gly Gly Met Lys Leu Met Thr Glu Thr Leu Ala Leu Glu Tyr
 165 170 175
 Ala Pro Lys Gly Ile Arg Val Asn Asn Ile Gly Pro Gly Ala Ile Asn
 180 185 190
 Thr Pro Ile Asn Ala Glu Lys Phe Ala Asp Pro Glu Gln Arg Ala Asp
 195 200 205
 Val Glu Ser Met Ile Pro Met Gly Tyr Ile Gly Glu Pro Glu Glu Ile
 210 215 220
 Ala Ala Val Ala Ala Trp Leu Ala Ser Ser Glu Ala Ser Tyr Val Thr
 225 230 235 240
 Gly Ile Thr Leu Phe Ala Asp Gly Gly Met Thr Gln Tyr Pro Ser Phe
 245 250 255
 Gln Ala Gly Arg Gly
 260

<210> 37

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
peptide

<400> 37

Trp Ile Ser Thr Lys Leu
1 5